

Supporting Information

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A A E P Y D E Q E E A S V E L P M E H R
CAGTGCATGAATACAAATCGAAGATCTGGGACAAAGCATTTAGCAACCAGGAGGCTATG
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Fig. S1. The nucleotide sequence of *c002* cDNA was used to BLAST the *Acyrtosiphon pisum* genomic reads at the Baylor College of Medicine Genome Sequencing Center (www.hgsc.bcm.tmc.edu/projects/aphid/). The 20 matching sequences were identified and assembled into two nonoverlapping contigs with the CAP3 Sequence Assembly Program [Huang X, Madan A (1999) CAP3: A DNA sequence assembly program. *Genome Res* 9:868–877]. The C002 coding region is divided into two exons with an intervening intron of >1.7 kb. The dotted line in the intron denotes the gap between the two contigs. Putative TATAA boxes are boxed in gray, and polyadenylation signal sequences (AATAAA) are underlined. The proximal poly(A) signal is likely to be the functional signal because this would give a transcript of the observed size.

